

Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, J. F., de Souza, S. J., and Simpson, A. T.
TITLE Shotgun sequencing of the human transcriptome with cRF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (7), 3491-3496 (2000)
MEDLINE 20:202663
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Profa. Auta de Souza, 4 andar, 01569-010, São Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.ox.ac.uk
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.ox.ac.uk/scripts/gcthm12.pl?pt1=RCT&t2=RCT-F104&2B0600-013-R001-2000-06-28&t4=1>
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 129.
FEATURES
 Source /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0046"
 /dev_staq="Adult"
 /note="Organ: lung-tumor; Vector: puc18; Site_1: small;
 Site_2: small; A mini-library was made by cloning products
 derived from ORBTEES PCK (U.S. letters patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
BASE COUNT 27 a 37 c 29 g 36 t
ORIGIN

High quality sequence start: 14
 High quality sequence stop: 129.
FEATURES
 Source /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0046"
 /dev_staq="Adult"
 /note="Organ: lung-tumor; Vector: puc18; Site_1: small;
 Site_2: small; A mini-library was made by cloning products
 derived from ORBTEES PCK (U.S. letters patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
BASE COUNT 27 a 37 c 29 g 36 t
ORIGIN

COMMENT contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 411 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 130.
FEATURES
SOURCE /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="AthRS RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide protein expression libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 49 a 21 c 27 g 33 t
ORIGIN

Alignment Scores:
 pred. No.: 1.0e+03
 Score: 28.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 12
 US-09-856-070-26 (1-5) x BG186686 (1-150)

Alignment Scores:
 pred. No.: 1.0e+03
 Score: 28.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 12
 US-09-856-070-26 (1-5) x BG186686 (1-150)

RESULT 3
 BG193987
LOCUS BG193987
DEFINITION RST13129 Athersys RAGE Library
VERSION BG193987.1
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 130)
AUTHORS Harrington, J. J., Sherr, B., Rundlett, S., Jackson, P. D., Petty, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Bozner, S., Mays, R., Smith, F., Veloso, N., Klika, A., Hess, J., Colbran, R., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 411 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 130.
FEATURES
SOURCE /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="AthRS RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 49 a 21 c 27 g 33 t
ORIGIN

cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances.

BASE COUNT 51 a 21 c 27 q 31 t

ORIGIN

Alignment Scores:
Pred. No.: 1.9e-03
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 12

(US-09-856-070-26 (1-5) x BG194087 (1-140)

QY 1 GlnAspTyrgluGlu 5
Lb 5b CAAGATTAAGAA; 80

ORIGIN

Length: 130
Matches: 5
conservative: 0
MisMatches: 0
Indels: 0
Gaps: 0

(US-09-856-070-26 (1-5) x BG194087 (1-140)

QY 1 GlnAspTyrgluGlu 5
Lb 5b CAAGATTAAGAA; 80

ORIGIN

Length: 140 bp mRNA linear EST 21-APP-2001
DEFINITION Homo sapiens cDNA, mRNA sequence.

QY 1 RST39188

Athersys RAGE library

EST

ORIGIN

Human. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 130)

Harrington,J.J., Shert,B., Bundlett,S., Jackson,P.D., Perry,R., Cain,S., Levitan,C., Thornton,M., Bachorowicz,A., Whittington,J., Lerner,I., Rosenthal,M., McElligott,K., Rozenzweig,S., May,P., Smith,E., Veloso,N., Kilkka,A., Hess,J., Cethren,K., Lo,K., Offenbacher,J.J., Banzing,J., and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)

ORIGIN

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scott@athersys.com

FEATURES

High quality sequence stop: 104.
Location/Qualifiers
1..130

source

/organism="Homo sapiens"

/clone.lib="Athersys RAGE library"

/note="See 'Creation of Genome-wide protein Expression

Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT

51 a 22 c 27 q 30 t

ORIGIN

(US-09-856-070-26 (1-5) x BG194087 (1-140)

QY 1 GlnAspTyrgluGlu 5
Lb 5b CAAGATTAAGAA; 80

ORIGIN

Length: 136 bp DNA linear EST 20-FEB-2002
DEFINITION BH719297

Lb 5b CAAGATTAAGAA; 80

ORIGIN

Accession: BH719297
Version: BH719297
Keywords: GSS

FEATURES

Organism: Brassica oleracea
Eukaryota; Vascular plants; Eudicots; core eudicots;
Rosidae; eudicots II; Brassicales; Brassicaceae; Brassica; oleracea.

REFERENCE

Authors: Town,C.D., Van Aken,S., Utterback,T., and Fraser,C.M.
Title: Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)

COMMENT

Other-GSS: BGMG267TF

CONTACT

Chris Town

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

Alignent Scores:
Pred. No.: 1.08e+03
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 12

FEATURES

Location/Qualifiers
1..136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

Alignent Scores:
Pred. No.: 1.08e+03
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17

FEATURES

Location/Qualifiers
1..136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

DNA is from a doubled haploid provided by Tom Osborn.

SEQUENCE

Seq primer: The

CLASS

sheared ends.

FEATURES

Source: /organism="Brassica oleracea"
/strain="TololiDm3"
/db_xref="TololiDm3"; 3712"
/clone="BGMG762"
/clone.lib="BG762"
/note="Vector: pBSL; Site_1: BstXI; Site_2: EcoRI; Site_3: KpnI"
/note="genomic DNA inserted into pBSL using BstXI linkers"

BASE COUNT

24 a 38 c 21 q 53 t

ORIGIN

(US-09-856-070-26 (1-5) x BH719297 (1-136)

FEATURES

Length: 136

REFERENCE

TIGR

COMMENT

FIELD	ITEM	DETAILS	REFERENCE
JOURNAL	TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression	J. J. Banaszak, J. and Thucar, M.
JOURNAL	NAME	Natl. Biotechnol.	Natl. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	CONTACT	Scott J. Cain	
COMMENT	Athersys, Inc.	3201 Carnegie Ave, Cleveland, OH 44115, USA	
COMMENT	TELEPHONE	216 431 9900	
COMMENT	FAX	216 361 9596	
COMMENT	EMAIL	Email: scain@athersys.com	
COMMENT	HIGH QUALITY SEQUENCE SOURCE	High quality sequence source: 137	
COMMENT	LOCATION/QUALIFIERS		
COMMENT	1. 137		
COMMENT	organism="Homo sapiens"		
COMMENT	db_xref="taxon:9606"		
COMMENT	clone_id="Athensys RAGE library"		
COMMENT	cell_line="HT1080"		
COMMENT	note="See 'Creation of Genome-wide protein expression libraries using random Activation of gene expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."		
SOURCE	SEQUENCE COUNT	33 a 31 c 23 g 50 t	

CONTACT Scott J. Cain
Althersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel: 216.431.9400
 Fax: 216.361.9596
 Email: scain@althersys.com
NATURES High quality sequence stop: 139.
source Local/Qualifiers 1..139
foranism="Homo sapiens"

/clone_lib="Athersys RAGE Library"
 /cell_line="H11080"
 /note="See 'Creation of genome-wide libraries using Random Activation of Nature Biotechnology', in press. Note cell type indicated is H11080, since method was used, these sequence tags expressed in H11080 under normal culture conditions."/>
 BASE COUNT 35 a
 ORIGIN 30 c
 23 q 50 t 1
 Alignment Scores:
 Pred. No.: 1.11e+03 Length: 1
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-109-855-070-25 {1-5} x HC192394 (1-139)
 QY 1 GluAspTyrGluGlu 5
 |||||
 TB 74 CAAGAGTACGAAAGAG 60
 RESULT 8
 BG193988/C
 LOCUS R:193988
 DEFINITION RST13140 Atherosclerosis-associated mRNA
 ACCESSION BG193988
 VERSION BG193988.1 G1:13715675
 KEYWORDS EST
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae
 REFERENCE 1 (bases 1 to 139)
 AUTHORS Harrington, L.J., Sherr, B., Rundlett, S., Jack, Cain, S., Leventhal, C., Thornton, M., Ramachandran, L., Lerner, L., Costanzo, D., McElligott, K., Horwitz, E., Veloso, N., Kilka, A., Hess, J., Crotham, K., Dazin, J., and Ducer, M.
 TITLE Creation of genome-wide protein expression library activation of gene expression
 JOURNAL Natl. Biotechnol. 19 (5): 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott, J. Cain
 Athersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel.: 216 361 9596
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 139.
 FEATURES source
 Source 1..139
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="H11080"
 /note="See 'Creation of genome-wide libraries using Random Activation of Nature Biotechnology', in press. Note cell type indicated is H11080, since method was used, these sequence tags expressed in H11080 under normal culture conditions."/>
 BASE COUNT 32 a
 ORIGIN 31 c
 23 q 53 t
 Alignment Scores:
 Pred. No.: 1.11e+03 Length: 13
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0

OS	09 856-070-26 {1-5} × BE170685 {1-148}	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 157)	
SY	1 GlnAspTyrGluGlu 5	REFERENCE 1	
Db	36 CAMIATTAGANAA 50	AUTHORS Kim, N.S., Hanin, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.F., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S., and Kim, Y.S.	
RESULT 1.1	RG192932	TITLE 21C Frontier Korean EST Project 2001	
COMMENT	RG192932	JOURNAL Unpublished (2002)	
ORGANISM	Homo sapiens	CONTACT Kim, Y.S.	
DEFINITION	RST12037 Athersys RAGE Library Human, sup, cDNA, mRNA seq, r	GENE Research Center	
VERSION	BG192942	Korea Research Institute of Bioscience & Biotechnology	
KEYWORDS	BG192942.1 GI:13714619	52 Eoju-dong Yuseong-gu, Daejeon 305-433, South Korea	
ORGANISM	Homo sapiens	tel: +82-42-860-4470	
COMMENT		FAX: +82-42-860-4409	
FEATURES		Email: yongsung@mail.kribb.re.kr	
SOURCE		Plate: 93 row: F column: 08	
FEATURES		High quality sequence stop: 157.	
LOCATION/QUALIFIERS		Location/Qualifiers 1..157	
FEATURES		Organism="Homo sapiens"	
LOCATION/QUALIFIERS		/db_xref="taxon:9606"	
FEATURES		/clone.lib="Athersys RAGE Library"	
LOCATION/QUALIFIERS		/note="See 'Creation of genome-wide Protein Expression	
FEATURES		Libraries using Random Activation of Gene Expression",	
LOCATION/QUALIFIERS		Nature Biotechnology, in press. Note that even though the	
FEATURES		cell type indicated is HT1080, since a random activation	
LOCATION/QUALIFIERS		method was used, these sequence tags are not necessarily	
FEATURES		expressed in HT1080 under normal circumstances."	
BASE COUNT	62 a 24 c 30 q 38 t	BASE COUNT 61 a 30 c 32 q 34 t	
ORIGIN		ORIGIN	
ALIGNMENT SCORES:		ALIGNMENT SCORES:	
PRED. NO.:	1.31e+03	PRED. NO.:	1.31e+03
SCORE:	28.00	SCORE:	28.00
PERCENT SIMILARITY:	100.00%	PERCENT SIMILARITY:	100.00%
BEST LOCAL SIMILARITY:	100.00%	BEST LOCAL SIMILARITY:	100.00%
QUERY MATCH:	100.00%	QUERY MATCH:	100.00%
DB:	14	DB:	14
	0S-09-856-070-26 (1-5) × RM844888 (1-157)		0S-09-856-070-26 (1-5) × RM844888 (1-157)
SY	1 GlnAspTyrGluGlu 5	SY	1 GluAspTyrGluGlu 5
Db	71 CAACATACGACAG 85	DB	39 CACGATATGAAAGAA 53
RESULT 1.2		RESULT 1.3	
DEFINITION	BMR44888	DEFINITION	MR1-SN0045-080400-001-002 SN0035 Homo sapiens cDNA, mRNA sequence.
LOCUS	BMR44888	LOCUS	AW867176
DEFINITION	K EST1124964 S12SN0126 q3 F9R e	DEFINITION	AW867176
VERSION	mRNA sequence.	VERSION	AW867176..1 C:18301228 EST.
KEYWORDS		KEYWORDS	human
VERSION	RM844888..1 GI:19201287	ORGANISM	Homo sapiens
KEYWORDS	FST	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
SOURCE	human	REFERENCE	{ bases 1 to 159 }
ORGANISM	Homo sapiens		

